

Practitioner's Docket No. MPI00-633P1RM**USSN 09/939,853****IN THE SPECIFICATION**

Please replace the paragraph at page 12, beginning at line 13 with the following paragraph:

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. See, *e.g.*,

<http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/> BLAST educational information provided by the National Center for Biotechnology Information (NCBI), Bethesda, MD.

Please replace the paragraph at page 15, beginning at line 1 with the following paragraph:

The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (<http://www.ebi.ac.uk/interpro> maintained by the European Bioinformatics Institute, Hinxton, Cambridge, UK). DOMAIN results for NOV1 as disclosed in Tables 1F, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections.

Please replace the paragraph at page 21, beginning at line 23 with the following paragraph:

The presence of identifiable domains in NOV2, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (<http://www.ebi.ac.uk/interpro> maintained by the European Bioinformatics Institute, Hinxton, Cambridge, UK). DOMAIN results for NOV2 as disclosed in Tables 1E, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections.

Please replace the paragraph at page 62, beginning at line 10 with the following paragraph:

The presence of identifiable domains in NOV8, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (<http://www.ebi.ac.uk/interpro> maintained by the European

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Bioinformatics Institute, Hinxton, Cambridge, UK). DOMAIN results for NOV8 as disclosed in Tables 1E, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections.

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